

IN THE SPECIFICATION

At page 2, line 24 through page 3, line 7, please replace the paragraph with the following text:

Accordingly, in one aspect, the invention features a nucleic acid molecule which encodes a 47324 protein or polypeptide, e.g., a biologically active portion of the 47324 protein. In a preferred embodiment, the isolated nucleic acid molecule encodes a polypeptide having the amino acid sequence of SEQ ID NO:2. In other embodiments, the invention provides an isolated 47324 nucleic acid molecule having the nucleotide sequence shown in SEQ ID NO:1, ~~SEQ ID NO:3, or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number _____~~. In still other embodiments, the invention provides nucleic acid molecules that are substantially identical (e.g., naturally occurring allelic variants) to the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, ~~or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number _____~~. In other embodiments, the invention provides a nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, ~~or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number _____~~, wherein the nucleic acid encodes a full length 47324 protein or an active fragment thereof.

At page 3, line 24 through page 4, line 2, please replace the paragraph with the following text:

In other embodiments, the invention provides 47324 polypeptides, e.g., a 47324 polypeptide having the amino acid sequence shown in SEQ ID NO:2; ~~the amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC Accession Number _____~~; an amino acid sequence that is substantially identical to the amino acid sequence shown in SEQ ID NO:2; or an amino acid sequence encoded by a nucleic acid molecule having a nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, ~~or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number _____~~, wherein the nucleic acid encodes a full length 47324 protein or an active fragment thereof.

At page 5, line 28 through page 6, line 22, please replace the paragraphs with the following text:

Figure 5a-b depicts a BLAST alignment of human 47324 with a consensus amino acid sequence derived from a ProDomain No. PD314684, "CG15399" (Release 2001.1; <http://www.toulouse.inra.fr/prodom.html>). The lower sequence is amino acid residues 69 to 234 and 12 to 61 of the 242 amino acid consensus sequence (SEQ ID NOs:6 and 7), while the upper amino acid

sequence corresponds to the "CG15399" domain of human 47324, amino acid residues 35 to 209 and 7 to 52 of SEQ ID NO:2.

Figure 6 depicts a BLAST alignment of human 47324 with a consensus amino acid sequence derived from a ProDomain No. PD302329, "CG4789" (Release 2001.1; <http://www.toulouse.inra.fr/prodom.html>). The lower sequence is amino acid residues 19 to 140 of the 155 amino acid consensus sequence (SEQ ID NO:8), while the upper amino acid sequence corresponds to the "CG4789" domain of human 47324, amino acid residues 121 to 231 of SEQ ID NO:2.

Figure 7 depicts a BLAST alignment of human 47324 with a consensus amino acid sequence derived from a ProDomain No. PD301653, "GB|AAF03448.1" (Release 2001.1; <http://www.toulouse.inra.fr/prodom.html>). The lower sequence is amino acid residues 80 to 135 of the 152 amino acid consensus sequence (SEQ ID NO:9), while the upper amino acid sequence corresponds to the "GB|AAF03448.1" domain of human 47324, amino acid residues 6 to 63 of SEQ ID NO:2.

Figure 8 depicts a BLAST alignment of human 47324 with a consensus amino acid sequence derived from a ProDomain No. PD000015, "GTP-binding lipoprotein prenylation transport Ras-related factor initiation ADP-ribosylation small family" (Release 2001.1; <http://www.toulouse.inra.fr/prodom.html>). The lower sequence is amino acid residues 7 to 222 of the 229 amino acid consensus sequence (SEQ ID NO:10), while the upper amino acid sequence corresponds to the "GTP-binding lipoprotein prenylation transport Ras-related factor initiation ADP-ribosylation small family" domain of human 47324, amino acid residues 8 to 225 of SEQ ID NO:2.

At page 7, line 26 through page 8, line 4, please replace the paragraphs with the following text:

For general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al. (1997) *Protein* 28:405-420 and <http://www.psc.edu/general/software/package/pfam/pfam.html>.

~~A plasmid containing the nucleotide sequence encoding human 47324 was deposited with American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA 20110-2209, on _____ and assigned Accession Number _____. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. This deposit was made merely as a convenience for those of skill in the art and is not an admission that a deposit is required under 35 U.S.C. §112.~~

At page 9, lines 16-29, please replace the paragraph with the following text:

To identify the presence of a “Ras family” domain in a 47324 protein sequence, and make the determination that a polypeptide or protein of interest has a particular profile, the amino acid sequence of the protein can be searched against a database of HMMs (e.g., the Pfam database, release 2.1) using the default parameters (http://www.sanger.ac.uk/Software/Pfam/HMM_search). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for MILPAT0063 and a score of 15 is the default threshold score for determining a hit. Alternatively, the threshold score for determining a hit can be lowered (e.g., to 8 bits). A description of the Pfam database can be found in Sonhammer et al., (1997) *Proteins* 28(3):405-420 and a detailed description of HMMs can be found, for example, in Gribskov et al., (1990) *Meth. Enzymol.* 183:146-159; Gribskov et al., (1987) *Proc. Natl. Acad. Sci. USA* 84:4355-4358; Krogh et al., (1994) *J. Mol. Biol.* 235:1501-1531; and Stultz et al., (1993) *Protein Sci.* 2:305-314, the contents of which are incorporated herein by reference.

At page 9, line 30 through page 10, line 11, please replace the paragraph with the following text:

A 47324 polypeptide can include an “ADP-ribosylation factor family domain” or regions homologous with a “ADP-ribosylation factor family domain”. As used herein, the term “ADP-ribosylation factor family domain” includes an amino acid sequence of about 100-250 amino acid residues in length and having a bit score for the alignment of the sequence to the ADP-ribosylation factor family domain (HMM) of at least 8. Preferably, an ADP-ribosylation factor family domain includes at least about 150-250 amino acids, more preferably about 175-250 amino acid residues, or about 200-225 amino acids and has a bit score for the alignment of the sequence to the ADP-ribosylation factor family domain (HMM) of at least 16 or greater. The ADP-ribosylation factor family domain (HMM) has been assigned the PFAM Accession PF00025 (<http://pfam.wustl.edu/>). An alignment of the ADP-ribosylation factor family domain (amino acids 2 to 206 of SEQ ID NO:2) of human 47324 with a consensus amino acid sequence derived from a hidden Markov model is depicted in Figure 3.

At page 10, lines 12-22, please replace the paragraph with the following text:

Preferably, the ADP-ribosylation factor family domain includes the following amino acid consensus sequence having Prosite signatures as PS01316, or sequences homologous thereto: E-x(5)-G-x-[SAG]-x(2)-[IV]-x-D-[LIV]-x(2)-[ST]-G-x-T-[LM] (SEQ ID NO:11). In the above conserved motif, and other motifs described herein, the standard IUPAC one-letter code for the amino acids is used. Each

element in the pattern is separated by a dash (-); square brackets ([]) indicate the particular residues that are accepted at that position; x indicates that any residue is accepted at that position; and numbers in parentheses (()) indicate the number of residues represented by the accompanying amino acid. The ADP-ribosylation factor family domain corresponds to about amino acids 2-206 of SEQ ID NO:2. The ADP-ribosylation factor family domain (HMM) has been assigned the PFAM Accession Number PF00025 (<http://genome.wustl.edu/Pfam/.html>).

At page 10, line 28 through page 11, line 7, please replace the paragraph with the following text:

A 47324 polypeptide can also include a "Ras family domain" or regions homologous with a "Ras family domain". As used herein, the term "Ras family domain" includes an amino acid sequence of about 100-250 amino acid residues in length and having a bit score for the alignment of the sequence to the Ras family domain (HMM) of at least 8. Preferably, a Ras family domain includes at least about 100-250 amino acids, more preferably about 150-250 amino acid residues, or about 200-225 amino acids and has a bit score for the alignment of the sequence to the Ras family domain (HMM) of at least 16 or greater. The Ras family domain (HMM) has been assigned the PFAM Accession PF00071 (<http://pfam.wustl.edu/>). An alignment of the Ras family domain (amino acids 8 to 231 of SEQ ID NO:2) of human 47324 with a consensus amino acid sequence derived from a hidden Markov model is depicted in Figure 4.

At page 11, lines 13-28, please replace the paragraph with the following text:

An additional method to identify domains in a 47324 protein sequence, and make the determination that a polypeptide or protein of interest has a particular profile, the amino acid sequence of the protein can be searched against a SMART database (Simple Modular Architecture Research Tool, <http://smart.embl-heidelberg.de/>) of HMMs as described in Schultz *et al.* (1998), *Proc. Natl. Acad. Sci. USA* 95:5857 and Schultz *et al.* (2000) *Nucl. Acids Res* 28:231. The database contains domains identified by profiling with the hidden Markov models of the HMMer2 search program (R. Durbin *et al.* (1998) *Biological sequence analysis: probabilistic models of proteins and nucleic acids*. Cambridge University Press.; <http://hmmer.wustl.edu/>). The database also is extensively annotated and monitored by experts to enhance accuracy. A search was performed against the HMM database resulting in the identification of an "AAA_5" domain in the amino acid sequence of human 47324 at about residues 29 to 241 of SEQ ID NO:2; a "rab_sub_5" domain in the amino acid sequence of human 47324 at about residues 7-187 of SEQ ID NO:2; a "ras_sub_4" domain in the amino acid sequence of human 47324 at about residues 4-209 of

SEQ ID NO:2; a “rho_sub_3” domain in the amino acid sequence of human 47324 at about residues 9-183 of SEQ ID NO:2(see Figure 1).

At page 12, line 7 through page 13, line 6, please replace the paragraphs with the following text:

A BLAST search was performed against the HMM database resulting in the identification of regions homologous to ProDom family PD314684(“CG15399” SEQ ID NO:6 and 7, ProDomain Release 2001.1; <http://www.toulouse.inra.fr/prodom.html>). An alignment of the “CG15399” domain (amino acids 35-209 and 7-52 of SEQ ID NO:2) of human 47324 with consensus amino acid sequences (SEQ ID NOs:6 and 7) derived from a hidden Markov model is depicted in Figures 5a and 5b. The consensus sequence for SEQ ID NO:6 is 25% identical over amino acids 35 to 209 and for SEQ ID NO:7 is 44% identical over amino acids 7 to 52 of SEQ ID NO:2 as shown in Figures 5a and 5b.

A BLAST search was performed against the HMM database resulting in the identification of regions homologous to ProDom family PD302329(“CG4789” SEQ ID NO:8, ProDomain Release 2001.1; <http://www.toulouse.inra.fr/prodom.html>). An alignment of the “CG4789” domain (amino acids 121-231 of SEQ ID NO:2) of human 47324 with consensus amino acid sequences (SEQ ID NO:8) derived from a hidden Markov model is depicted in Figure 6. The consensus sequence for SEQ ID NO:8 is 43% identical over amino acids 121 to 131 of SEQ ID NO:2 as shown in Figure 6.

A BLAST search was performed against the HMM database resulting in the identification of regions homologous to ProDom family PD301653(“GB|AAF03448.1” SEQ ID NO:9, ProDomain Release 2001.1; <http://www.toulouse.inra.fr/prodom.html>). An alignment of the “GB|AAF03448.1” domain (amino acids 6-63 of SEQ ID NO:2) of human 47324 with consensus amino acid sequences (SEQ ID NO:9) derived from a hidden Markov model is depicted in Figure 7. The consensus sequence for SEQ ID NO:9 is 44% identical over amino acids 6 to 63 of SEQ ID NO:2 as shown in Figure 7.

A BLAST search was performed against the HMM database resulting in the identification of regions homologous to ProDom family PD000015(“GTP-binding lipoprotein prenylation transport Ras-related factor initiation ADP-ribosylation small family” SEQ ID NO:10, ProDomain Release 2001.1; <http://www.toulouse.inra.fr/prodom.html>). An alignment of the “GTP-binding lipoprotein prenylation transport Ras-related factor initiation ADP-ribosylation small family” domain (amino acids 8-225 of SEQ ID NO:2) of human 47324 with consensus amino acid sequences (SEQ ID NO:10) derived from a hidden Markov model is depicted in Figure 8. The consensus sequence for SEQ ID NO:10 is 21% identical over amino acids 8 to 225 of SEQ ID NO:2 as shown in Figure 8.

At page 23, lines 5-29, please replace the paragraphs with the following text:

A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of 47324 (e.g., the sequence of SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~) without abolishing or more preferably, without substantially altering a biological activity, whereas an "essential" amino acid residue results in such a change. For example, amino acid residues that are conserved among the polypeptides of the present invention, e.g., those present in the Ras family domain, are predicted to be particularly unamenable to alteration.

A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a 47324 protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a 47324 coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for 47324 biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

At page 25, lines 1-14, please replace the paragraph with the following text:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within a sequence identity or homology

limitation of the invention) is using a Blossum 62 scoring matrix with a gap open penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

At page 25, lines 19-31, please replace the paragraph with the following text:

The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al., (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 47324 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to 47324 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>.

At page 27, line 20 through page 29, line 2, please replace the paragraphs with the following text:

In one embodiment, an isolated nucleic acid molecule of the invention includes the nucleotide sequence shown in SEQ ID NO:1, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~, or a portion of any of these nucleotide sequences. In one embodiment, the nucleic acid molecule includes sequences encoding the human 47324 protein (i.e., "the coding region", from nucleotides 19-729 of SEQ ID NO:1, including the terminal codon), as well as 5' untranslated sequences (nucleotides 1-18 of SEQ ID NO:1). Alternatively, the nucleic acid molecule can include only the coding region of SEQ ID NO:1 (e.g., nucleotides 19-729 of SEQ ID NO:1, corresponding to SEQ ID NO:3) and, e.g., no flanking sequences which normally accompany the subject sequence. In another embodiment, the nucleic acid molecule encodes a sequence corresponding to the mature protein of SEQ ID NO:2.

In another embodiment, an isolated nucleic acid molecule of the invention includes a nucleic acid molecule which is a complement of the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~, or a portion of any of these nucleotide sequences. In other embodiments, the nucleic acid molecule of the invention is sufficiently complementary to the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC~~

as Accession Number _____ such that it can hybridize to the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC~~ as Accession Number _____; thereby forming a stable duplex.

In one embodiment, an isolated nucleic acid molecule of the present invention includes a nucleotide sequence which is at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more homologous to the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC~~ as Accession Number _____. In the case of an isolated nucleic acid molecule which is longer than or equivalent in length to the reference sequence, e.g., SEQ ID NO:1, or SEQ ID NO:3, the comparison is made with the full length of the reference sequence. Where the isolated nucleic acid molecule is shorter than the reference sequence, e.g., shorter than SEQ ID NO:1, or SEQ ID NO:3, the comparison is made to a segment of the reference sequence of the same length (excluding any loop required by the homology calculation).

47324 Nucleic Acid Fragments

A nucleic acid molecule of the invention can include only a portion of the nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC~~ as Accession Number _____. For example, such a nucleic acid molecule can include a fragment which can be used as a probe or primer or a fragment encoding a portion of a 47324 protein, e.g., an immunogenic or biologically active portion of a 47324 protein. A fragment can comprise: nucleotides 40-711 of SEQ ID NO:1, which encodes a Ras family domain of human 47324. The nucleotide sequence determined from the cloning of the 47324 gene allows for the generation of probes and primers designed for use in identifying and/or cloning other 47324 family members, or fragments thereof, as well as 47324 homologues, or fragments thereof, from other species.

At page 29, lines 17-25, please replace the paragraph with the following text:

47324 probes and primers are provided. Typically a probe/primer is an isolated or purified oligonucleotide. The oligonucleotide typically includes a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, 12 or 15, preferably about 20 or 25, more preferably about 30, 35, 40, 45, 50, 55, 60, 65, or 75 consecutive nucleotides of a sense or antisense sequence of SEQ ID NO:1, ~~SEQ ID NO:3, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC~~ as Accession Number _____, or of a naturally occurring allelic variant or mutant of SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC~~ as Accession Number _____.

At page 30, line 12 through page 31, line 11, please replace the paragraphs with the following text:

A nucleic acid fragment encoding a "biologically active portion of a 47324 polypeptide" can be prepared by isolating a portion of the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~, which encodes a polypeptide having a 47324 biological activity (e.g., the biological activities of the 47324 proteins as described herein), expressing the encoded portion of the 47324 protein (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the 47324 protein. For example, a nucleic acid fragment encoding a biologically active portion of 47324 includes a Ras family domain (e.g., about nucleotides 40-711 of SEQ ID NO:1). A nucleic acid fragment encoding a biologically active portion of a 47324 polypeptide, may comprise a nucleotide sequence which is greater than 300-1200 or more nucleotides in length.

In preferred embodiments, nucleic acids include a nucleotide sequence which is about 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400 nucleotides in length and hybridizes under stringent hybridization conditions to a nucleic acid molecule of SEQ ID NO:1, or SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~.

47324 Nucleic Acid Variants

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~. Such differences can be due to degeneracy of the genetic code (and result in a nucleic acid which encodes the same 47324 proteins as those encoded by the nucleotide sequence disclosed herein). In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence which differs, by at least 1, but less than 5, 10, 20, 50, or 100 amino acid residues that shown in SEQ ID NO:2. If alignment is needed for this comparison the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.

At page 31, lines 23-28, please replace the paragraph with the following text:

In a preferred embodiment, the nucleic acid differs from that of SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~, e.g., as follows: by at least one but less than 10, 20, 30, or 40 nucleotides; at least one but less than 1%, 5%,

10% or 20% of the in the subject nucleic acid. If necessary for this analysis the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.

At page 32, lines 20-23, please replace the paragraph with the following text:

Moreover, nucleic acid molecules encoding other 47324 family members and, thus, which have a nucleotide sequence which differs from the 47324 sequences of SEQ ID NO:1, SEQ ID NO:3, ~~or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~ are intended to be within the scope of the invention.

At page 65, line 30 through page 66, line 8, please replace the paragraph with the following text:

The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length 47324 nucleic acid, such as the nucleic acid of SEQ ID NO:1, ~~or the DNA insert of the plasmid deposited with ATCC as Accession Number _____~~, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to 47324 mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays are described herein.